



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:
Nadejda G. Gurskaya, et al.

Serial No.: 10/501,629

Confirmation No.: 9951

Filed: July 15, 2004

**For: NOVEL FLUORESCENT
PROTEIN FROM AEQUOREA
COERULSCENS AND
METHODS FOR USING THE
SAME**

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Group Art Unit: 1656

Examiner: Maryam Monshipouri

MAIL STOP AMENDMENT
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

CERTIFICATE OF MAILING
37 CFR 1.8

I hereby certify that this correspondence is being deposited with sufficient postage as first class mail in an envelope addressed to: Mail Stop Amendment, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450 on

3/28/2008

Keith M. Tackett

Typed Name

32.008

Reg. No. if applicable

Kunz

Signature

(713) 623-4844

Telephone Number

DECLARATION UNDER 37 C.F.R. §1.132

I, Sergey Lukyanov, hereby declare and state that:

1. I am a scientist at Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry (Moscow, Russia), Evrogen JSC, and I am one of the inventors of the subject application.
2. I have worked in the molecular biology field for 22 years.
3. I have a Ph.D. degree in Molecular Biology from 1993 and a D.Sc. degree in Molecular Biology from 1999.
4. I declare that I have read the specification of United States Patent Application Serial No. 10/501,629 (the '629 application), filed July 15, 2004, the pending claims and the final Office Action dated January 23, 2008.

5. Paragraphs [00105] and [00106] of the '629 application describe a MegAlign algorithm used to determine "sequence identity."
6. The MegAlign clustal algorithm described in the '629 application is calculated by comparing two optimally aligned sequences, determining the number of positions at which the identical amino acid occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions, and multiplying the result by 100. The MegAlign algorithm accounts for all mismatches, without preference, regardless of whether or not the mismatch is a conserved mismatch.
7. As used in the '629 application, common understanding of the term "sequence identity" also requires comparing two optimally aligned sequences, determining the number of positions at which the identical amino acid occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions, and multiplying the result by 100.
8. Based on the description in the '629 application, the claim language "at least 96% identical" is understood to be determined by the following equation:
$$(\text{number of amino acid matches}) / (\text{total number of amino acids}) * 100.$$
9. Attachments 3 and 4 of the final Office Action identify a "Query Match" term and a "Best Local Similarity" term. The "Query Match" term does not consider conservative mismatches equivalent to other mismatches. As an example, Attachment 3 identifies "Length 238" and "Matches 221" such that $(\text{number of amino acid matches}) / (\text{total number of amino acids}) * 100$ is:
$$221 / 238 * 100 = 92.9\% \text{ (the same as the "Best Local Similarity").}$$
10. Sequences shown in Attachments 3 and 4 of the final Office Action are respectively only 92.9% and 91.2% identical to SEQ ID NO: 2 referenced in claim 1 of the '629 application, and thereby are not "at least 96% identical to the *Aequorea coerulescens* non-fluorescent protein of SEQ ID NO: 2," as recited in claim 1.

The undersigned, Sergey Lukyanov, hereby declares that all statements made herein of my own knowledge are true and that these statements made on information and belief are believed to be true and further that these statements were made with knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of this application or any patent resulting therefrom.

Date: March, 27, 2008

Signature: _____



SEQUENCE LISTING

<110> Gurskaya, Nadejda
Fradkov, Arkadiy
Lukyanov, Sergey
Punkova, Natalia

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 ctgtccacac aatctgccct ttccaaagat cccaacgaaa agagagatca catgatcctg 660
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 <212> PRT
 <213> Aequoria coerulescens

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				85					90					95			
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			100					105					110				
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Ser	Arg	Ile	Glu	Leu	Thr	Gly	Thr		
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	130					135					140						
Tyr	Asn	Ala	Thr	Asn	Val	Tyr	Ile	Met	Thr	Asp	Lys	Ala	Lys	Asn	Gly		
145				150					155						160		
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Lys	Asp	Gly	Ser	Val		
			165					170						175			
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro		
			180					185					190				
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser		
	195					200					205						
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Ile	Tyr	Phe	Glu	Phe	Val		
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<212> DNA

<213> *Aequoria coerulescens*

<400> 21

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gtcactactc tctcttatgg tgttcaatgc ttttcaagat atccagatca tatgaaacag 240
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gaagatgacg ggaactacaa gtcgcgtgct gaagtcaagt tgcagggtga taccctgggt 360
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cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga taaccattac 600
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<210> 22

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<213> *Aequoria coerulescens*

<400> 22

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			20					25					30				
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		

	35					40					45						
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu		
	50					55					60						
Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln		
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His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Ile	Gln	Glu	Arg		
				85					90					95			
Thr	Ile	Phe	Phe	Glu	Asp	Asp	Gly	Asn	Tyr	Lys	Ser	Arg	Ala	Glu	Val		
			100					105					110				
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Thr	Gly	Thr		
			115					120					125				
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	Asn	Lys	Met	Glu	Tyr	Asn		
	130					135					140						
Tyr	Asn	Ala	Ser	Asn	Val	Tyr	Ile	Met	Thr	Asp	Lys	Ala	Lys	Asn	Gly		
145					150					155					160		
Ile	Lys	Val	Asn	Leu	Lys	Ile	Arg	His	Asn	Ile	Ala	Asp	Gly	Ser	Val		
			165						170					175			
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro		
			180					185					190				
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser		
			195				200					205					
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Ile	Tyr	Phe	Glu	Phe	Val		
	210					215				220							
Thr	Ala	Ala	Ala	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Ile	Lys				
225					230					235							

<210> 23

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<212> DNA

<213> Aequoria coerulescens

<400> 23

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<210> 24

<211> 238

<212> PRT

<213> Aequoria coerulescens

<400> 24

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			20					25				30					
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		

		35				40				45							
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu		
	50					55					60						
Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln		
65					70					75					80		
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Ile	Gln	Glu	Arg		
				85					90					95			
Thr	Ile	Phe	Phe	Glu	Asp	Asp	Gly	Asn	Tyr	Lys	Ser	Arg	Ala	Glu	Val		
				100				105					110				
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Thr	Gly	Thr		
	115						120					125					
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	Asn	Lys	Met	Glu	Tyr	Asn		
	130					135					140						
Tyr	Asn	Ala	His	Asn	Val	Tyr	Ile	Met	Thr	Asp	Lys	Ala	Lys	Asn	Gly		
145					150					155					160		
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val		
				165					170					175			
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro		
			180					185					190				
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser		
	195						200					205					
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Ile	Tyr	Phe	Gly	Phe	Val		
	210					215					220						
Thr	Ala	Ala	Ala	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys				
225						230					235						

<210> 25

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<212> PRT

<213> Aequoria coerulescens

<400> 25

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			20					25					30				
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		
			35				40					45					
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe		
	50					55					60						
Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln		
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His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		
				85					90					95			
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
				100				105					110				
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		
	115						120					125					
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		
	130					135					140						
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly		
145					150					155					160		
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val		
				165					170					175			
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro		
			180					185					190				

